

Genome Sequence of *Blastococcus saxobsidens* DD2, a Stone-Inhabiting Bacterium

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Members of the genus *Blastococcus* have been isolated from sandstone monuments, as well as from sea, soil, plant, and snow samples. We report here the genome sequence of a member of this genus, *Blastococcus saxobsidens* strain DD2, isolated from below the surface of a Sardinian wall calcarenite stone sample.

The genus *Blastococcus*, an actinobacterium in the order *Frankiales* (8), comprises three species, isolated from sea (1) and soil and plant (9) samples but most emblematically from stones (10). The species *Blastococcus saxobsidens*, comprising strains isolated from calcareous stones, was described in 2004 (11). Relative to *Modestobacter* and *Geodermatophilus*, the other genera grouped with it in the family *Geodermatophilaceae* (7), it is prevalent in the interior of the stones according to a study on Sardinian calcarenites (4, 11). It is also found in dust uplifted from desert locales and deposited as snow on the Alps (2) or on the Himalayas (12).

Its morphology is unusual for an actinobacterium, with coccoid cells aggregated in tetrads, buds that give the genus its name, and orange-pigmented irregular colonies. Its physiology, still poorly characterized, is also unusual with thermophilic esterases (3) and resistance to several metals higher than those of its phylogenetic relatives; conversely, its resistance to several oxidizing stresses was much lower (4). It is able to grow aerobically on a limited range of sugars. It is still unclear how it manages to thrive in such inhospitable and bleak biotopes as the interior of stones, and this was the rationale for determining its genome sequence.

Blastococcus saxobsidens strain DD2 was isolated from a sample harvested below the surface of a calcarenite stone from a crumbling wall in Cagliari, Sardinia (11). The strain was grown on complex Luedemann's medium (5).

The finished genome of DD2 was generated using a combination of Sanger and 454 (6) technologies. Around 20× coverage of 454 GSflx reads was mixed with 4× coverage of Sanger reads for the scaffolding, issued from a 10-kb insert fragment size library. The assembly was done using Newbler (Roche) and validated via the Consed interface (www.phrap.org). To improve assembly scaffolding, around 5× coverage of 454 mate-paired GSflx reads, with a 3-kb insert size, was added.

For the finishing phases, primer walking on clones and transposon "bombings" were realized, yielding a single contig molecule without gaps.

The genome sequence of *Blastococcus saxobsidens* DD2 has 4,875,340 bp with a GC content of 72.95%. It has a single circular chromosome with 5,078 genes, of which 4,845 encode proteins, 57 encode structural RNAs, including three 16S-23S-5S operons, and

233 represent pseudogenes. Several genes were found in multiple copies, such as *arsBC* (arsenite resistance), *copC* (copper resistance protein), *coxSML* (carbon monoxide dehydrogenase), *czcD* (cobalt-zinc-cadmium resistance), *dnaG* (DNA primase), *recQ* (DNA helicase), *soxABDG* (sarcosine oxidase), *trwC* (conjugative relaxase), and *uvrA* and *uvrD* (UV resistance).

Nucleotide sequence accession number. The *Blastococcus saxobsidens* DD2 genome sequence and annotation data have been deposited in the EMBL under accession number [F0117623](https://www.ebi.ac.uk/EMBL/ accession/F0117623).

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